



DORMANCY-RELATED TRANSCRIPT ACCUMULATION OF THE DEHYDRIN GENE FAMILY IN APPLE BUDS

Miotto, YE¹; Falavigna, VS²; Porto, DD³; Margis-Pinheiro, M²; Pasquali, G²; Revers, LF^{3*}

¹Engenharia de Bioprocessos e Biotecnologia, Univ. Estadual do Rio Grande do Sul, Bento Gonçalves, RS, 95700-000. ²Programa de Pós-Graduação em Biologia Celular e Molecular, Centro de Biotecnologia, Univ. Fed. do Rio Grande do Sul, Porto Alegre, RS, 91501-970.

³Laboratório de Genética Molecular Vegetal, Embrapa Uva e Vinho, Bento Gonçalves, RS, 95700-000.

*E-mail: luis.revers@embrapa.br

Keywords: bud dormancy, dehydrin, gene expression, *Malus x domestica*, RT-qPCR.

Dormancy and cold acclimation are fundamental processes of plant survival in environments undergoing seasonal low temperatures. Dormancy can be defined as the inability to initiate growth from meristem under favorable conditions. This phenomenon is responsible for growth cessation, leaf senescence and establishment of dormant buds. Regulation of these processes in perennial plants such as apple (*Malus x domestica* Borkh.) involves the induction of protective mechanisms including the accumulation of cryoprotective molecules. In a previous study, our group had identified differentially expressed genes during apple bud dormancy, including transcripts coding for dehydrins (DHNs). DHNs are proteins that accumulate in response to cold stress, acting in the protection of cellular lipid membranes and cryoprotective mechanisms. In apple, nine *DHN* genes were identified and their expressions were related to different abiotic stress responses. This work aimed to deepen our knowledge about the relationships of the *DHN* genes and the bud dormancy process in apple trees. The consensus sequence of the conserved K segment from DHNs was used for BLASTP searches in the apple genome database. Deduced DHN amino acid sequences from apple, *Arabidopsis*, rice, barley, grapevine and poplar were used to construct a cladogram inferred by Mr. Bayes software. For transcript accumulation analysis, total RNA was extracted from closed buds of the 'Fuji Standard' apple cultivar sampled in eight different dates of 2009/2010. Complementary DNAs were synthesized for gene expression analysis by RT-qPCR. Four novel *DHN* genes (*MdDHN10-13*) were identified in the apple genome. Phylogenetic analysis revealed the presence of two clades composed solely by apple DHNs, all of them localized in chromosome 2. The remaining apple *DHNs* (four) were located in the other four chromosomes and grouped with *DHNs* from other species in the phylogenetic tree. This result allowed us to suggest the occurrence of gene duplication events in chromosome 2 that could explain the higher number of *DHNs* in this species. The *MdDHNs* showed a seasonal expression profile in closed buds, with transcript accumulation occurring mainly during winter. Although they showed a common expression pattern, some genes were more induced than others, suggesting that these genes may have different roles during bud dormancy progression in apple.

Financial support: CAPES, CNPq, EMBRAPA & FINEP.